

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (8 letters)

residues 66-73 of SEQ ID NO: 12

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|cl|87188

|cl|87188

Description

None

Molecule type

amino acid

Query Length

8

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Multiple alignment](#)] [NEW](#)

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.345924	0.294
K	0.292556	0.11
H	1.73538	0.61

Results Statistics

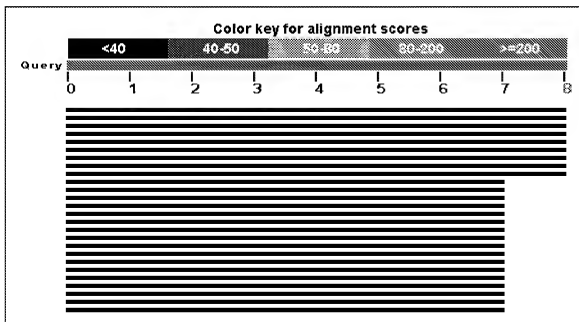
Length adjustment	0
Effective length of query	8
Effective length of database	3505793397
Effective search space	28046347176
Effective search space used	28046347176

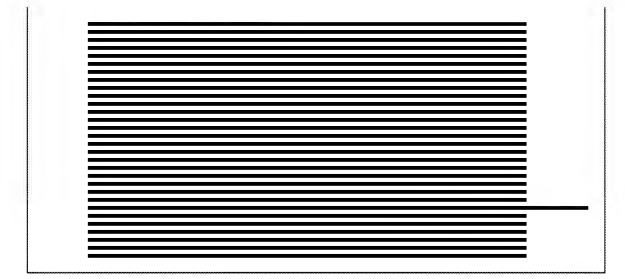
[Graphic Summary](#)[Show Conserved Domains](#)

No putative conserved domains have been detected

**Distribution of 100 Blast Hits on the Query Sequence**

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

E	Sequences producing significant alignments:	Score	Value
		(Bits)	
ref XP_014778592.1	hypothetical protein StAA4_07162 [Streptom...	25.2	708
ref XP_001353186.1	hypothetical protein An08g10820 [Aspergil...	25.2	708
ref NP_01461905.1	beta-lactamase [Stigmatella aurantiaca DW4...	25.2	708
gb AAJ1664.1	surface antigen [Hepatitis B virus]	25.2	708
ref NP_04382235.1	bifunctional protein [Rhodococcus erythrop...	24.8	949
ref YP_002764653.1	wax ester synthase/diacylglycerol acyltra...	24.8	949
gb EESE8299.1	conserved hypothetical protein [Toxoplasma gon...	24.8	949
gb EESE20499.1	conserved hypothetical protein [Toxoplasma gon...	24.8	949
ref NP_002370822.1	hypothetical protein TGME49_015010 [Toxop...	24.8	949
gb ACQ82751.1	S protein [Hepatitis B virus]	24.4	1274
gb ACQ82751.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACQ82750.1	large S protein [Hepatitis B virus]	24.4	1274
ref NP_04858486.1	conserved hypothetical protein [Ruminococc...	24.4	1274
gb BAU84154.1	hepatitis B surface antigen [Hepatitis B virus]	24.4	1274
gb BAU84102.1	hepatitis B surface antigen [Hepatitis B virus]	24.4	1274
gb BAU83930.1	hepatitis B surface antigen [Hepatitis B virus]	24.4	1274
gb ACJ66248.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66247.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66246.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66244.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66244.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66243.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66228.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66227.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66226.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66213.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66212.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66207.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66206.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66205.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66164.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66163.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66136.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66135.1	large S protein [Hepatitis B virus] >gb ACJ66...	24.4	1274
gb ACJ66130.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66129.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66128.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66127.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66096.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66095.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66081.1	large S protein [Hepatitis B virus] >gb ACJ660...	24.4	1274
gb ACJ66066.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66065.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66064.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66097.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66096.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66059.1	S protein [Hepatitis B virus]	24.4	1274
gb ACJ66058.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66057.1	large S protein [Hepatitis B virus]	24.4	1274
ref YP_002663239.1	putative methyltransferase [Methylobacter...	24.4	1274
gb ACR66188.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66183.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66182.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66180.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66170.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66160.1	large S protein [Hepatitis B virus]	24.4	1274

gb ACR66153.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66138.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66139.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66133.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66097.1	large S protein [Hepatitis B virus] >gb ACR661...	24.4	1274
gb ACR66094.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66096.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR66029.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR66001.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65996.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65994.1	large S protein [Hepatitis B virus] >gb ACR661...	24.4	1274
gb ACR65994.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65994.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65994.1	large S protein [Hepatitis B virus] >gb ACR659...	24.4	1274
gb ACR65994.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65932.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR65923.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR65920.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65903.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65891.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65894.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR65880.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR65876.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65869.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65859.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR65855.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65852.1	large S protein [Hepatitis B virus] >gb ACR659...	24.4	1274
gb ACR65840.1	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR65833.1	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACR65825.1	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACR65817.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65809.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65808.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR65807.1	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb XP_002579293.1	Upstream stimulatory factor [Schistosoma ...	24.4	1274
gb ACR20704.1	S protein [Hepatitis B virus]	24.4	1274
gb ACR20703.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACR20700.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR20564.1	S protein [Hepatitis B virus]	24.4	1274
gb ACR20563.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACR20560.1	large S protein [Hepatitis B virus]	24.4	1274
gb ACR20413.1	S protein [Hepatitis B virus]	24.4	1274
gb ACR20412.1	middle S protein [Hepatitis B virus]	24.4	1274
gb ACR20411.1	large S protein [Hepatitis B virus]	24.4	1274

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) **NEW**

>ref|ZP_05477858.1| hypothetical protein StAA4_07162 [Streptomyces sp. AA4]
Length=241

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPG+TR
Sbjct 70 PLIPGATR 77

>ref|XP_001393186.1| **G** hypothetical protein An08g10820 [Aspergillus niger]
emb|CAK45755.1| **G** unnamed protein product [Aspergillus niger]
Length=489

GENE ID: 4983396 An08g10820 | hypothetical protein

[Aspergillus niger CBS 513.88] (10 or fewer PubMed links)

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPG+TR
Sbjct 327 PLIPGTTR 334

>ref|ZP_01461905.1| beta-lactamase [Stigmatella aurantiaca DW4/3-1]
gb|EAF67348.1| beta-lactamase [Stigmatella aurantiaca DW4/3-1]
Length=392

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PL+PGSTR
Sbjct 294 PLVPGSTR 301

>gb|AAD13661.1| surface antigen [Hepatitis B virus]
Length=226

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPG+TR
Sbjct 108 PLIPGTTR 115

>ref|ZP_04388235.1| bifunctional protein [Rhodococcus erythropolis SK121]
gb|EEN84692.1| bifunctional protein [Rhodococcus erythropolis SK121]
Length=458

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 363 PLIPGSSR 370

>ref|YP_002764633.1| **G** wax ester synthase/diacylglycerol acyltransferase [Rhodococcus erythropolis PR4]
dbj|BAH31894.1| **G** putative wax ester synthase/diacylglycerol acyltransferase [Rhodococcus erythropolis PR4]
Length=458

GENE ID: 7714817 RER_11860 | wax ester synthase/diacylglycerol acyltransferase [Rhodococcus erythropolis PR4] (10 or fewer PubMed links)

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 363 PLIPGSSR 370

>gb|EEE28209.1| conserved hypothetical protein [Toxoplasma gondii VEG]
Length=417

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 181 PLIPGSSR 188

>gb|EEE20499.1| conserved hypothetical protein [Toxoplasma gondii GT1]
Length=405

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
 PLIPGS+R
 Sbjct 169 PLIPGSSR 176

>ref|XP_002370822.1| G hypothetical protein TGME49_015010 [Toxoplasma gondii ME49]
 gb|EEB03682.1| G hypothetical protein TGME49_015010 [Toxoplasma gondii ME49]
 Length=405

GENE ID: 7900763 TGME49_015010 | hypothetical protein [Toxoplasma gondii ME49]

Score = 24.8 bits (51), Expect = 949
 Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
 PLIPGS+R
 Sbjct 169 PLIPGSSR 176

>gb|ACQ82752.1| S protein [Hepatitis B virus]
 Length=226

Score = 24.4 bits (50), Expect = 1274
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
 PLIPGST
 Sbjct 108 PLIPGST 114

>gb|ACQ82751.1| middle S protein [Hepatitis B virus]
 Length=281

Score = 24.4 bits (50), Expect = 1274
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
 PLIPGST
 Sbjct 163 PLIPGST 169

>gb|ACQ82750.1| large S protein [Hepatitis B virus]
 Length=400

Score = 24.4 bits (50), Expect = 1274
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
 PLIPGST
 Sbjct 282 PLIPGST 288

>ref|ZP_04858486.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
 gb|EES75479.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
 Length=146

Score = 24.4 bits (50), Expect = 1274
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
 PLIPGST
 Sbjct 90 PLIPGST 96

>dbj|BAH84154.1| hepatitis B surface antigen [Hepatitis B virus]
 Length=132

Score = 24.4 bits (50), Expect = 1274
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
 PLIPGST
 Sbjct 69 PLIPGST 75

>dbj|BAH84102.1| hepatitis B surface antigen [Hepatitis B virus]
 Length=132

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 69 PLIPGST 75

>dbj|BAH83930.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 69 PLIPGST 75

>gb|ACJ66248.1| middle S protein [Hepatitis B virus]
Length=281

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 163 PLIPGST 169

>gb|ACJ66247.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 282 PLIPGST 288

>gb|ACJ66242.1| S protein [Hepatitis B virus]
Length=226

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 108 PLIPGST 114

>gb|ACJ66241.1| middle S protein [Hepatitis B virus]
Length=281

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 163 PLIPGST 169

>gb|ACJ66240.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
Sbjct 282 PLIPGST 288

>gb|ACJ66233.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)